RAW SEQUENCE LISTING
ERROR REPORT
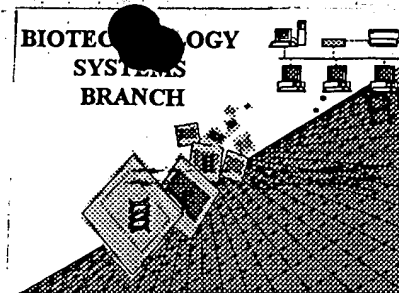
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/331,723*

Source: *1638*

Date Processed by STIC: *11-07-00*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

[X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

[ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

[ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

[X] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

[ ] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

[ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

[ ] 7. Other: _____

Applicant Must Provide:

[X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

[ ] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

[X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
   Technical Assistance......................................703-287-0200
   To Purchase PatentIn Software.......................703-306-2600

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```
      RAW SEQUENCE LISTING              DATE: 11/07/2000
      PATENT APPLICATION: US/09/331,723 TIME: 11:47:54

      Input Set : A:\PTO.txt
      Output Set: N:\CRF3\11072000\I331723.raw

 3 <110> APPLICANT: BOYNTON, John
 4        GILLHAM, Nicholas
 5        RANDOLPH-ANDERSON, Barbara
 6        ISHIGE, Fumiharu
 7        SATO, Ryo
 9 <120> TITLE OF INVENTION: METHODS OF CONFERRING PPO-INHIBITING HERBICIDE RESISTANCE IN PLANTS BY
10        GENE MANIPULATION
12 <130> FILE REFERENCE: 2185-156P
14 <140> CURRENT APPLICATION NUMBER: US 09/331,723
15 <141> CURRENT FILING DATE: 1999-08-18
17 <150> PRIOR APPLICATION NUMBER: PCT/US96/20415
18 <151> PRIOR FILING DATE: 1996-12-27
20 <160> NUMBER OF SEQ ID NOS: 24
22 <170> SOFTWARE: PatentIn version 3.0
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 47
26 <212> TYPE: PRT
27 <213> ORGANISM: Chlamydomonas reinhardtii
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30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: ()..()
32 <223> OTHER INFORMATION: Strain CC-407
35 <220> FEATURE:
36 <221> NAME/KEY: PEPTIDE
37 <222> LOCATION: (1)..(47)
38 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
41 <400> SEQUENCE: 1
43 Ala Ala Glu Ala Leu Gly Ser Phe Asp Tyr Pro Pro Val Gly Ala Val
44 1               5                   10                  15
46 Thr Leu Ser Tyr Pro Leu Ser Ala Val Arg Glu Glu Arg Lys Ala Ser
47             20                  25                  30
49 Asp Gly Ser Val Pro Gly Phe Gly Gln Leu His Pro Arg Thr Gln
50          35                  40                  45
52 <210> SEQ ID NO: 2
53 <211> LENGTH: 46
54 <212> TYPE: PRT
55 <213> ORGANISM: Arabidopsis thaliana
57 <220> FEATURE:
58 <221> NAME/KEY: misc_feature
59 <222> LOCATION: ()..()
60 <223> OTHER INFORMATION: ecotype Columbia
63 <220> FEATURE:
64 <221> NAME/KEY: PEPTIDE
65 <222> LOCATION: (1)..(46)
66 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
69 <400> SEQUENCE: 2
71 Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val
```

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Input Set : **A:\PTO.txt**
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```
72 1               5                  10                 15
74 Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp
75              20                 25                 30
77 Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln
78           35                 40                 45
80 <210> SEQ ID NO: 3
81 <211> LENGTH: 46
82 <212> TYPE: PRT
83 <213> ORGANISM: Zea mays
85 <220> FEATURE:
86 <221> NAME/KEY: misc_feature
87 <222> LOCATION: ()..()
88 <223> OTHER INFORMATION: Strain B73 inbred
91 <220> FEATURE:
92 <221> NAME/KEY: PEPTIDE
93 <222> LOCATION: (1)..(46)
94 <223> OTHER INFORMATION: product = porphyric herbicide resistance domain
97 <400> SEQUENCE: 3
99 Ala Ala Asp Ala Leu Ser Arg Phe Tyr Tyr Pro Pro Val Ala Ala Val
100 1               5                  10                 15
102 Thr Val Ser Tyr Pro Lys Glu Ala Ile Arg Lys Glu Cys Leu Ile Asp
103             20                 25                 30
105 Gly Glu Leu Gln Gly Phe Gly Gln Leu His Pro Arg Ser Gln
106           35                 40                 45
108 <210> SEQ ID NO: 4
109 <211> LENGTH: 141
110 <212> TYPE: DNA
111 <213> ORGANISM: Chlamydomonas reinhardtii
113 <220> FEATURE:
114 <221> NAME/KEY: misc_feature
115 <222> LOCATION: ()..()
116 <223> OTHER INFORMATION: Strain CC-407
119 <220> FEATURE:
120 <221> NAME/KEY: misc_feature
121 <222> LOCATION: (1)..(141)
122 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
125 <400> SEQUENCE: 4
126 gccgccgagg ccctgggctc cttcgactac ccgccggtgg gcgccgtgac gctgtcgtac        60
128 ccgctgagcg ccgtgcggga ggagcgcaag gcctcggacg ggtccgtgcc gggcttcggt       120
130 cagctgcacc cgcgcacgca g                                                 141
133 <210> SEQ ID NO: 5
134 <211> LENGTH: 138
135 <212> TYPE: DNA
136 <213> ORGANISM: Arabidopsis thaliana
138 <220> FEATURE:
139 <221> NAME/KEY: misc_feature
140 <222> LOCATION: ()..()
141 <223> OTHER INFORMATION: ecotype Columbia
144 <220> FEATURE:
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RAW SEQUENCE LISTING   DATE: 11/07/2000
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Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\11072000\I331723.raw**

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146 <222> LOCATION: (1)..(138)
147 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
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153 ccgaaagaag caatccgaac agaatgtttg atagatggtg aactaaaggg ttttgggcaa     120
155 ttgcatccac gcacgcaa                                                   138
158 <210> SEQ ID NO: 6
159 <211> LENGTH: 138
160 <212> TYPE: DNA
161 <213> ORGANISM: Zea mays
163 <220> FEATURE:
164 <221> NAME/KEY: misc_feature
165 <222> LOCATION: ()..()
166 <223> OTHER INFORMATION: Strain B73 inbred
169 <220> FEATURE:
170 <221> NAME/KEY: misc_feature
171 <222> LOCATION: (1)..(138)
172 <223> OTHER INFORMATION: encodes porphyric herbicide resistance domain
175 <400> SEQUENCE: 6
176 gctgcagatg ctctatcaag attctattat ccaccggttg ctgctgtaac tgtttcgtat      60
178 ccaaaggaag caattagaaa agaatgctta attgatgggg aactccaggg ctttggccag     120
180 ttgcatccac gtagtcaa                                                   138
183 <210> SEQ ID NO: 7
184 <211> LENGTH: 36
185 <212> TYPE: DNA
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
189 <221> NAME/KEY: misc_feature
190 <222> LOCATION: (1)..(36)
191 <223> OTHER INFORMATION: Oligonucleotide primer for Arabidopsis thaliana
194 <400> SEQUENCE: 7
195 ctatattacc caccaatggc agcagtatct atctcg                               36
198 <210> SEQ ID NO: 8
199 <211> LENGTH: 38
200 <212> TYPE: DNA
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <221> NAME/KEY: misc_feature
205 <222> LOCATION: (1)..(38)
206 <223> OTHER INFORMATION: Oligonucleotide primer for Zea mays
209 <400> SEQUENCE: 8
210 gattctatta tccaccgatg gctgctgtaa ctgtttcg                             38
213 <210> SEQ ID NO: 9
214 <211> LENGTH: 26
215 <212> TYPE: PRT
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <221> NAME/KEY: misc_feature
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Input Set : **A:\PTO.txt**
Output Set: **N:\CRF3\11072000\I331723.raw**

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220 <222> LOCATION: ()..()
221 <223> OTHER INFORMATION: Oligonucleotide primer common to both of A. thaliana and Z. mays
222       p
225 <220> FEATURE:
226 <221> NAME/KEY: misc_feature
227 <222> LOCATION: ()..()
228 <223> OTHER INFORMATION: "n" residues can be inosine in addition to G, A, T or C; "k" at p
229       o
232 <400> SEQUENCE: 9
234 Lys Ala Tyr Thr Ala Tyr Cys Cys Asn Cys Cys Asn Ala Thr Gly Gly
235 1               5                   10                  15
237 Ser Asn Gly Cys Asn Gly Thr Asn Trp Ser
238                 20                  25
240 <210> SEQ ID NO: 10
241 <211> LENGTH: 2573
242 <212> TYPE: DNA
243 <213> ORGANISM: Chlamydomonas reinhardtii
245 <220> FEATURE:
246 <221> NAME/KEY: misc_feature
247 <222> LOCATION: ()..()
248 <223> OTHER INFORMATION: Strain RS-3
251 <220> FEATURE:
252 <221> NAME/KEY: misc_feature
253 <222> LOCATION: (1)..(2573)
254 <223> OTHER INFORMATION: encodes protoporphyrinogen oxidase
257 <400> SEQUENCE: 10
258 ctcgagagcg ttggaggaaa tccgtttggc acctgttccg gcttctttgt gtgcacggcc    60
260 acgtcccct ttcctgctac ccgctccccc ccggctttac tgcccttcc actcctcggc    120
262 tccatcccga ttccatccgc tcctcctccc ccacctagac tgtctaccgt ctaccagttt    180
264 cttgggcaat cattaacgta acccgcctc cctgcgcctg cccctccctc cctctccccc    240
266 ccgcacagcc cgccgccgcc gaggccctgg gctccttcga ctacccgccg atgggcgccg    300
268 tgacgctgtc gtacccgctg agcgccgtgc gggaggagcg caaggcctcg gacggqtccg    360
270 tgccgggctt cggtcagctg cacccgcgca cgcaggtggg caagtgcgag cgtgttgcgg    420
272 gcggtgtgtt gcggagggga gggtggtggg ggttggggt gggggtgggg gggattgggg    480
274 cgctgggtcg tatcccgcgg ttgtatcctc gcgctccct catccattcc ccccttcaac    540
276 aacacacacg ggcgcacacg caccctcttt gcgcttactt tgtctggtgc tccttaacac    600
278 actcttcgct tcattttggt gtcttctaac acacacactt gtccacacac agggcatcac    660
280 cactctgggc accatctaca gctccagcct gttccccggc cgcgcgcccg agggccacat    720
282 gctgctgctc aactacatcg gcggcaccac caaccgcggc atcgtcaacc agaccaccga    780
284 gcagctggtg gagcaggtgt gtgtgtgggg gggtgggggg ggggcagtgg atttttgggc    840
286 tgagcccccct gagcaaagcg atccaggggg ggcgaagccc cccaggattg ccccctgtccg    900
288 tgcgtgcgtg tgtgcctgtg tcgacaaaaa gtaccgtact ggcacaaacc gcgagtgcca    960
290 cgtattatta attgcaatta cctattgtag aaaaatagac ggcagggaaa actcggccgg    1020
292 agcgagaagc gacctcgtga gtccatggac atcttgactt tcttcagttc gcgagtatag    1080
294 ctctcggccc ctaaatatct tacatccatg tatcaaaaca tgtcgacgac aagcgtcttg    1140
296 gggcaagaat gtcgaaattg tttgcaacag ccaaaccatg cgtccccgag ccttacatgt    1200
298 gtcgcggccc gggatcccgc gcccgagccc ggctagccct ttgcggtgct tgagtgggat    1260
300 gtgggtgagg tgcatttggg atatcatgga ccgtgaagtg gcgtgggtaa ggtggcgtgg    1320
302 cgtggcgggg acagggcatg tcggtgcctc ggcacagcgt tggcctagtg gccagtcccg    1380
```

?

This is an
amino acid
sequence.

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304 ctggatgggc ttgcaagggt gctgttcatg tcgccggtgc ccatcgtcac atccccttgc    1440
306 gctacatggg gctcagccca tttccagct gtacaaagct gacacccctt gttgtgtggc     1500
308 gtcttggacc cgtgttgctt cggagctggc cagaacccc tgtgggcaca cacacgcaca     1560
310 cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca cacacacaca    1620
312 cacacacaca cacacacaca cacacacaca cacacacaca cacattttcg tcctgcagcc    1680
314 ccgaaccccg ccgcccgttc cacgtcttcc acctgccgca cccccccccc tgccgcacgc    1740
316 ctgctctcac cgcctctccc cccaccccat ctccctgcag gtggacaagg acctgcgcaa    1800
318 catggtcatc aagcccgacg cgcccaagcc ccgtgtggtg ggcgtgcgcg tgtggccgcg    1860
320 cgccatcccg caggtgtgag ggcgcagcag ccggagggat gggctagatc ctagtttctc    1920
322 aaagagctct acagccctat aacctcgacc tgcgaccttc gacctgataa cctggctgcc    1980
324 ccctcccaac ctagccacct ctccccggat ttgggttcac tcggttgact tgcttttggg    2040
326 ttctggaatc aacttcacct gttgtatact ttgctgcact tctctgtacc actctttgca    2100
328 ttaggttcgg tttagtttgg gctgcatgtg taacccctcc tccccgccct gccacctgca    2160
330 gttcaacctg ggccacctgg agcagctgga caaggcgcgc aaggcgctgg acgcggcggg    2220
332 gctgcagggc gtgcacctgg ggggcaacta cgtcagcggt gagcgcgtgg gcagcagcag    2280
334 cagcaggaag aggggagggg aggggagggg aggtacaag gaggaggttg agcaggaggt     2340
336 ggtgctaagg cgcaaagcaa ggcggtgttg tatcctcatt gactgaaacc gggaaaccca    2400
338 gcatgaacaa gaggtcaggg gactgcaagg agcggaggct acatgtatga ctaccccga     2460
340 cgcgggcgat gattccttga ctattgggac ctatttcgtt gggctcgggc acatgacccc    2520
342 cctggccccct tcgctgtatg gtgcccagcc gcccagccgc cccccgccca cac          2573
345 <210> SEQ ID NO: 11
346 <211> LENGTH: 1704
347 <212> TYPE: DNA
348 <213> ORGANISM: Arabidopsis thaliana
350 <220> FEATURE:
351 <221> NAME/KEY: misc_feature
352 <222> LOCATION: ()..()
353 <223> OTHER INFORMATION: ecotype Columbia
356 <220> FEATURE:
357 <221> NAME/KEY: CDS
358 <222> LOCATION: (16)..(1629)
359 <223> OTHER INFORMATION: product = protoporphyrinogen oxidase
362 <400> SEQUENCE: 11
363 ttctctgcga tttcc atg gag tta tct ctt ctc cgt ccg acg act caa tcg     51
364                 Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser
365                  1               5                   10
367 ctt ctt ccg tcg ttt tcg aag ccc aat ctc cga tta aat gtt tat aag     99
368 Leu Leu Pro Ser Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys
369         15                  20                  25
371 cct ctt aga ctc cgt tgt tca gtg gcc ggt gga cca acc gtc gga tct    147
372 Pro Leu Arg Leu Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser
373     30                  35                  40
375 tca aaa atc gaa ggc gga gga ggc acc acc atc acg acg gat tgt gtg    195
376 Ser Lys Ile Glu Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val
377 45                  50                  55                  60
379 att gtc ggc gga ggt att agt ggt ctt tgc atc gct cag gcg ctt gct    243
380 Ile Val Gly Gly Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala
381                 65                  70                  75
383 act aag cat cct gat gct gct ccg aat tta att gtg acc gag gct aag    291
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VERIFICATION SUMMARY   DATE: 11/07/2000
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